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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 694 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                           May 14, 2002, 04:24:33 ; Search time 75.1 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-998-416-633
US-08-232-463-14
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US-08-404-615-3
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US-08-340-4348-2
US-08-124-394A-21
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Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Wenchile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
MUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996 ATTORNEX/AGENT INFORMATION:
                               US-08-326-119A-24
US-08-88-219B-5
US-09-233-35A-5
US-09-402-035-5
US-08-960-780-3
US-08-960-780-3
US-08-960-780-3
US-08-971-988-3
US-08-471-044-28
US-08-471-044-28
US-08-471-046A-28
US-08-471-046A-28
US-08-471-046A-28
                     -09-057-762-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
BUDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          Sequence 741, Application US/08998416 Patent No. 6239264
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
GENERAL INFORMATION:
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

TELECHORE: 919-541-8687

INFORMATION FOR SEQ ID NO: 633:

SEQUENCE CHARACTERISTICS:
                                            COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin PATENT PATENT
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ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 50.3
Matches 280; Conservative
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Polimann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                Length
                                                                                                                                                                                        0; Mismatches 274; Indels
                                                                                                                DB 4;
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                    Score 147.6;
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Patent No. 6239264
GENERAL INFORMATION:
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                                                                                                                                                    Best_Local Similarity 54.6
Matches 344; Conservative
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                                                             6
4.3%; Score 90.2; DB 4; Length 711; 50.3%; Pred. No. 1.4e-19; 1.ve 0; Mismatches 268; Indels
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Wed May 15 08:05:15 2002

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1736 aagtggttcgaaaacgagctacaatggcttaaggagaaatcttgtgaagtctctgtcatc 1795
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                      847 caacccettcatcccaatcaccggattgagctttagtactttcaacttttaccacaaatg 906
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                                                                                                907 gtcagcatacgtctgcttcatgttagccgtcgtccattcaatcgttatgaccgcttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
SUFTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.9%; Score 39.2; DB 1; Best Local Similarity 2.2%; Pred. No. 0.042; Matches 8; Conservative 200; Mismatches 148;
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 899149 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , CLONE: pTZgpt-Fls
US-08-232-463-14
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TOPOLOGY: lir
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2.3%; Score 48.6; DB 1; Length 77
Best Local Similarity 3.4%; Pred. No. 3.4e-05;
Matches 12; Conservative 203; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                    APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: FECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30472/114 IMMU
                                                                                                                                                                                                                                                                                                          1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BERT, STEPPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                            Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
551 GAAAGCTACACCTGGTA 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                               STATE: VA
COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                            US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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359 aagacagttgtttcacaaccgttgatggcaaatgagacggcctatcactactatgag 418
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                                                                                                           754 CATTTATGTGCCTTGCTGATCATGAAGGAATATAAAGGGGATTAGATGAGCTGTTTCTT 813
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Pred. No. 1.7;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08404665
Patent No. 5591583
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Hemperly, Ohn J.
TITLE OF INVENTION: SEQUENCES
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/404,665

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: FUGIT, Donna R.

REFERENCE/DOCKET NUMBER: 32,135

REGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.68;
54.98;
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Best Local Similarity 54.9
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1 Becton Driv
CITY: Franklin Lakes
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
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US-08-404-665-3
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US-08-404-671-3/c
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US-08-404-665-3/c
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                                                                                                           1976 ggaccagcgactttcaatgacgactttaggaatgcagttgtacaaggtatcgattctagt 2035
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                                                                                                                                                                                                                                                                           2036 ctgaagatagatgtcgaactagaggaggaggagttttacttggtaagagctcaagct 2091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Mirkov, T. Erik
APPLICANT: Mirkov, T. Erik
TITLE OF INVINION: Protection of Plants Against Pathogens
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fitch, Even, Tabin & Flannery STREET: 135 South LaSalle Street, Suite 900 CITY: Chicago CATAE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy alsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWRARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/798,223A
FILING DATE: 1991125
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/762,679
FILING DATE: 19-SEP-1991
ATTORNEY,AGENT INFORMATION:
NAME: Seldman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/POCKET NUMBER: 31,79
REFERENCE/POCKET NUMBER: 51984
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TENGTH: 964 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07798223A Patent No. 5422108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
25..459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-07-798-223A-1
                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-07-798-223A-1
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APPLICANT: Typfer, R., Bautor, J., Bothmann, H., Filsak, E.,
APPLICANT: Hvricke-Grandpierre, C., Klein, B., Martini, N.,
APPLICANT: Miler, A., Schulte, W., Voetz, M., Walek, J.,
APPLICANT: Schell, J.
TITLE OF INVENTION: Promoters
NUMBER OF SEQUENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 1; Length 4724;
Pred. No. 1.7;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPETING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Steinberg, Raskin & Davidson, P.C. STREET: 1140 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,860B
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02950
FILING DATE: 05-SEP-1994
APPLICATION NUMBER: DE P4329951.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08617860B Patent No. 6133506
                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/POCKET UNMER: P-334
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4724 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.6
Best Local Similarity 54.9
Matches 67; Conservative
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                07417
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                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.6%; Score 34; DB 1; Length 4724; Best Local Similarity 54.9%; Pred. No. 1.7; Matches 67; Conservative 0; Mismatches 55; Indels
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Sequence 3, Application US/08404781
Patent No. 5681931
Patent No. 5681931
PAPLICANT: Reid, Robert A.
PAPLICANT: Acid, Robert A.
PAPLICANT: Hemperly, John J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                              APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
                                                                                                                                                                                                                              ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,671
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-334
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4724 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Sequence 3, Application US/08404671
Patent No. 5635360
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                      07417
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1694 TT 1693
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3350 TACAGGAAGGCACATGAAATTGAAGGCAACATGGTTGCGCACCTTGTGCATGTTCTT 3291
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1.6%; Score 33.6; DB 2; Length 4706;
Best Local Similarity 55.0%; Pred. No. 2.2;
Matches 66; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08331081B
Patent No. 5998697
GENERAL INFORMATION:
APPLICANT: Devlin, Robert H.
TITLE OF INVENTION: Transgenic Fish and Vectors Therefor NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: McFadden, Fincham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUTY: Ottawa
STATE: Ontario
COUNTR: Canada
ZIP: K2P 1P9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb
MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM PC or Compatibles
OPERATING SYSTEM: PC Dos 5.0
SOFFWARE: Wordperfect 5.1 (Patseq.txt)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,081B
FILING DATE: October 20, 1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: Canada 2,126,138
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      enzyme sites and signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 Metcalfe Street, Suite 606
                                           NAME: Fincham, H. Ian
REGISTRATION NUMBER: 26,375
REFERENCE/DOCKET NUMBER: 5478-1A
TELECOMMUNICATION INPORMATION:
TELEPHONE: (613) 234-1907
TELEFAX: (613) 234-5233
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fincham, H. Ian
REGISTRATION NUMBER: 26,375
REFERENCE/DOCKET NUMBER: 5478-1A
                                                                                                                                                                                                                                                                                                                                                        1-6 for ECORI
325-330 for BamHI
4084-4089 for XbaI
4391-4396 for Poly-A
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FILING DATE: June 17, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (613) 234-1907
TELEFAX: (613) 234-5233
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                          LENGTH: 4706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-331-081B-3/c
                                                                                                                                                                                                                                                                                                                                                        LOCATION:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-08-331-081B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.6%; Score 33.6; DB 3; Length 4450; Best Local Similarity 55.0%; Pred. No. 2.1; Matches 66; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Devlin, Robert H.
TITLE OF INVENTION: Transgenic Fish and Vectors Therefor NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: McFadden, Fincham
STREET: 225 Metcalfe Street, Suite 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Octawa
SIATE: Octawa
ZIP: K2P 1P9
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb
MEDIUM TYPE: Biskette 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM PC or Compatibles
OPERATING SYSTEM: PC Dos 5.0
SOFTWARE: Wordperfect 5.1 (Patseq.txt)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,081B
FILING DATE: October 20, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: Canada 2,126,138
                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4450 base pairs TYPE: Nucleic acid STRANDEDNESS: double stranded TOPOLOGY: linear MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-331-081B-5/c
equence 5, Application US/08331081B
Patent No. 5998697
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        LIBRARY: genomic Lambda FIX II
CLONE: BnACCaseg1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription start 3367
                                                                                                                                                                                                   ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Brassica napus
IMMEDIATE SOURCE:
  04-SEP-1993
                                                                                                                                                                                                                                                                                                                                                        CAAT-Signal
3124..3127
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4089..4091
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4089..4421
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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FEATURE:
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US-08-617-860B-2
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US-08-476-008-43
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                                                                                                                                                                                                                          364 agttgtttcacaaccgttgatggcaaatgagacggcctatcactactactgaggaaaa 423
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application US/08476008

Patent No. 5627061

GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 69
CORRESPONDENCE: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    ;
0
                                                                                                                                            Score 33.6; DB 2; Length 4744;
                                                                                                                                                                                    54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCFWAREN STATEM: TO LOSTED DOS SCFWAREN SPECIAL ON VERSION #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: HOERNER Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (314)537-6047
INFONATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                          1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
LENGTH: 4744 base pairs
                                                                                                                                                                                  66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                       nucleic acid
                                                             linear
                                                                                                                                                           Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: St. Louis
STATE: Missouri
                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63198
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STREET: 70
                                                             ; TOPOLOGY:
US-08-331-081B-3
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                                                                                                                                                                                                                                                                                          430 gatccacttgaatttgatgcgatctcaatggtgcgcatggggcctcgtcttcttctgggt 489
                                                                                                                                                                                                                                                                                                                                  824 GCGGTAATATCCAACTTTTCAATCAAACAACTGGTGCTGAACCTACTGCTTCTATTCGTA 883
                                                                                                                                                                                                                                                                                                                                                                                                                                       884 TTCAATACACACCAATGCTTCAACCAATAACAATCGAAGGAGAATTAGTTCCAAAAGCAA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       550 tatggcaaattctgttaagaagtctcttatctacccaagcgtttacaaagactacaacga 609
                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          490 egcagteettacegeegeaactatettgaacatteteaaaegegtatteggeaagaacat
                                                                                                  Length 1293;
                                                                                             Score 32.8; DB 1; Length 1
Pred. No. 1.7;
0; Mismatches 132; Indels
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STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28 AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31 AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
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; Sequence 43, Application US/08306063
; Patent No. 5633435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
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                                                                                               1.6%;
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                                                                                               Query Match
Best Local Similarity 45.9
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
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                                                                                                                                      NAME: HOEFIGE JF., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMUNICATION IMPORMATION:
TELEPHONE: (314)737-6099
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOEFIGE Jr., Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                            LENGTH: 1293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Missouri
COUNTRY: USA
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US-08-833-485-43
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CITY: St
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Patent No. 5804425
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,485
FILING DATE: O7.APR-1997
CLASSIFFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13.5EP-1994
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Palace
         INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                            SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-306-063-43
                                                                                                                        TOPOLOGY:
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      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                    NAME: HOETNEY INCOMENTATION:
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6097
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/33,485
FILING DATE: US 08/33,485
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US 07/75,537
FILING DATE: 31-AUG-1990
ATTORNEY AGENT INFORMATION:
ANDE: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY AGENT INFORMATION:
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 1.1293
US-09-137-440-43
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/product= "Fe3+-reductase"
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AAF58254
AAF58257
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20..2080
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  99WO-JP01481
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    AAZ59028
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CDS
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**SIDSI / gcgdata/geneseq, NA1981. DAT:*

**SIDSI / gcgdata/geneseq, NA1984. DAT:*

**SIDSI / gcgdata/geneseq, NA1984. DAT:*

**SIDSI / gcgdata/geneseq, NA1986. DAT:*

**SIDSI / gcgdata/geneseq, NA1986. DAT:*

**SIDSI / gcgdata/geneseq, NA1980. DAT:*

**SIDSI / gcgdata/geneseq, Geneseqn, NA1981. DAT:*

**SIDSI / gcgdata/geneseq, Geneseqn, NA1998. DAT:*

**SIDSI / gcgdata/geneseq, Geneseqn, NA1998. DAT:*

**SIDSI / gcgdata/geneseq, Geneseqn, NA1998. DAT:*

**SIDSI / gcgdata/geneseq, Geneseqn, NA1999. DAT:*

**SIDSI / gcgdata/geneseq, Geneseqn, NA1999. DAT:*

**SIDSI / gcgdata/geneseq/geneseqn, NA1999. DAT:*

              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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The invention relates to a method of transforming a higher plant with a foreign gene in which the polyadenylation signal region contained in the nucleotide sequence of the foreign gene has been modified by nucleotide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene used is especially an iron (Pe) 3+ (ferric) reductase gene in which putative polyadenylation signals contained within the coding sequence are substituted with alterative codons for expression in higher plants. This sequence represents a plant codon optimised version of the wild type yeast ferric reductase (FREI gene). The sequence has had putative polyadenylation signal and poly(A) addition sites removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired foreign gene, especially to improve iron absorption efficiency in crop
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The invention relates to a method of transforming a higher plant with a foreign gene in which the polyademylation signal region contained in the nucleotide sequence of the foreign gene has been modified by nucleotide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene expression product is not substantially impaired. The foreign gene expression product is contained within the coding sequence are substituted with alterative contained within the coding sequence are substituted with alterative contained within the coding sequence are substituted with alterative wild type yeast ferric reductase (FRRI gene). The plant codon-optimised gene has had putative polyademylation signal and poly(A) addition sites removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired foreign gene, especially to improve iron absorption efficiency in crop plants.
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Pred. No. 5.2e-16;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 26 C; 13 G; 27 T; 0 other;
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100.0%; Pred
0; }
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BP,
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83
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                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
  DNA;
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83; Conserv
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AAZ59031 standard;
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Best Local S:
Matches 83
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                                                                                 Crop plant; polyadenylation signal; substitution; ferric reductase; iron; yeast; heterologous gene; ss.
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                                                                                                                                                                                                                                                            Yamaguchi H;
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                                                                                                                                                                                                                                                                                                                                     6; 81pp; Japanese.
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AA259032 standard; DNA; 83 BP.
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Matches 83; Conservative
                                                                                                                   Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                            Nakanishi H,
                                                                                                                                                                                                                                                                                WPI; 1999-571924/48
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                                        11-APR-2000
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AAZ59033
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polyadenylation signal; substitution; ferric reductase; iron;
                                                             Crop plant; polyadenylation signal; substitution; ferric reductase; iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a foreign gene in which the polyadenylation signal region optical the nucleotide substitution to give a sequence not having this function, in such exception to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene used is especially an iron (Fe) 3+ (ferric) reductase gene in which putative polyadenylation signals contained within the coding sequence are substituted with alterative codons for expression in higher plants. Oligonuleotides AAZ59031-259060 were used as overlapping oligonucleotide primers to generate a plant codon-optimised yeast ferric reductase (FRE) addition sites are removed by nucleotide substitution. The method allows the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a method of transforming a higher plant with
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Oligonucleotide A-3 for generating codon-optimised ferric reductase.
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ches 0;
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ID AAZ59034 standard; DNA; 83
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Best Local Similarity 100.C
Matches 83; Conservative
                                                                                                                                                            Saccharomyces cerevisiae. Synthetic.
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polyadenylation signal; substitution; ferric reductase; iron;
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Pred. No. 5.2e
0; Mismatches
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100.0%; Prer
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ID AA259035 standard; DNA; 83 BP.
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               Saccharomyces cerevisiae. Synthetic.
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Best Local Simi
Matches 83;
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The invention relates to a method of transforming a higher plant with a foreign gene in which the polyadenylation signal region contained in the uncleotide sequence of the foreign gene modified by nucleotide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene expression product is not substantially impaired. The foreign gene expression product is not substantially impaired. The foreign gene substituted with a lighbar contained within the coding sequence are substituted with a large coding for expression in higher plants. Oilgonuleotides AAZ5901-Z55060 were used as overlapping oilgonucleotide primers to generate a plant codon-optimised yeast ferric reductase (FREI gene; AAZ59028) in which putative polyadenylation signal and poly(A) addition incless are removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired foreign gene, especially to improve iron absorption efficiency in crop Transformation of higher plant with foreign gene having modified Sequence 83 BP; 18 A; 15 C; 20 G; 30 T; 0 other; Yamaguchi H; (NISC-) JAPAN SCI & TECHNOLOGY CORP. Disclosure; Fig 6; 81pp; Japanese. Ok1 H, 99WO-JP01481 98JP-0096637 Nakanishi H, WPI; 1999-571924/48. poly(A) site 24-MAR-1999; 24-MAR-1998; 30-SEP-1999. Mori S, 

ö Length 83; Indels 4.0%; Score 83; DB 20; L 100.0%; Pred. No. 5.2e-16; ive 0; Mismatches 0; 83; Conservative Query Match Best Local Similarity Matches

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282 tttacacactggaggacatgaagaacatctaccttaatgcaagtaactaccttcgcgctc 341 ò 염

342 ctgagaaatccgataagaagaca 364 23 CTGAGAAATCCGATAAGAAGACA 1 ò

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Gaps

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AAZ59036/c ID AAZ59036 standard; DNA; 83 BP. (first entry) 11-APR-2000 AAZ59036;

Crop plant; polyadenylation signal; substitution; ferric reductase; iron; yeast; heterologous gene; ss. Oligonucleotide A-6 for generating codon-optimised ferric reductase. Saccharomyces cerevisiae 

WO9948356-A1. 30-SEP-1999 Synthetic

99WO-JP01481.

24-MAR-1999;

98JP-0096637

24-MAR-1998;

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                                                                                                                                                                                                             The invention relates to a method of transforming a higher plant with a foreign gene in which the polyadenylation signal region contained in the nucleotide sequence of the foreign gene has been madified by nucleotide substitution to give a sequence not having this function in such a way that the function of the foreign gene expression product is not substantially impalred. The foreign gene used is especially an iron (Fe) 3+ (ferric) reductase gene in which putative polyadenylation signals contained within the coding sequence are substituted with alterative codons for expression in higher plants. Oligonuleotides ALS9001-25906 were used as overlapping oligonucleotide primers to generate a plant codon-optimised yeast ferric reductase (FREI gene; ARZ59028) in which putative polyadenylation signal and poly(A) addition sites are removed by nucleotide substitution. The method allows the
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                                                                                                                                 Transformation of higher plant with foreign gene having modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 83 BP; 19 A; 19 C; 17 G; 28 T; 0 other;
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                                                               Yamaguchi
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                              (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                Disclosure; Fig 6; 81pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 ctatgaggaaaactatgggatcc 434
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                                                               Ok1 H,
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                                                               Nakanishi H,
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Best Local Similarity
                                                                                               WPI; 1999-571924/48.
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                                                                                                                                                  poly(A) site
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The invention relates to a method of transforming a higher plant with a foreign gene in which the polyadenylation signal region contained in the uncleotide sequence of the foreign gene modified by nuclectide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene expression product is not substantially impaired. The foreign gene used is especially an iron signals contained within the coding sequence are substituted with alterative codons for expression in which putative polyadenylation signal score used as overlapping oil gonuclectide primers to generate a plant codon optimised yeast ferric reductase (FRRI gene; AAZ59031, an which putative polyadenylation signal and poly(A) addition gites are removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired foreign gene, especially to improve iron absorption efficiency in crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crop plant; polyadenylation signal; substitution; ferric reductase; iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                             Transformation of higher plant with foreign gene having modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 83;
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100.0%; Pred. No. 5.2e-16;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 83 BP; 22 A; 26 C; 12 G; 23 T; 0 other;
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                                                                                               Disclosure; Fig 6; 81pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 acaaatggtcagcatacgtctgc 83
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Best Local Similarity 100.0
Matches 83; Conservative
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            WPI; 1999-571924/48.
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                                                                 poly(A) site
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a foreign gene in which the polyadenylation signal region contained in uncleotide sequence of the foreign gene has been modified by nucleotide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene used is especially an iron (Feb 3+ ferric) reductase gene in which putative polyadenylation signals contained within the coding sequence are substituted with alterative codons for expression in higher plants. Oligonuleotides AAZ59031-259060 were used as overlapping oligonucleotide primers to generate a plant codon optimised yeast ferric reductase (FREI gene; AAZ59028) in which putative polyadenylation signal and poly(A) addition sites are removed by nucleotide substitution. The method allows the foreign of transformant plants with improved expression of a desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyadenylation signal; substitution; ferric reductase; iron;
                                                                                                                                                                                                                                                         foreign gene, especially to improve iron absorption efficiency in crop
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              Fig 6; 81pp; Japanese
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Best Local Simi
Matches 83;
              Disclosure;
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The invention relates to a method of transforming a higher plant with a foreign gene in which the polyadenylation signal region contained in

Transformation of higher plant with foreign gene having modified poly(A) site -

Disclosure; Fig 6; 81pp; Japanese.

poly(A) site

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Gaps

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Crop plant; polyadenylation signal; substitution; ferric reductase; iron; yeast; heterologous gene; ss.
           nucleotide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene used is especially an iron (Fe) 3+ (ferric) reductase gene in which putative polyadenylation signals contained within the coding sequence are substituted with alterative codons for expression in higher plants. Oligonuleotides AAS59031-259660 were used as overlapping oligonucleotide primers to generate a plant codon-optimised yeast ferric reductase (FREI gene; AAS59028) in which putative polyadenylation signal and poly(a) addition sites are removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide C-4 for generating codon-optimised ferric reductase.
nucleotide sequence of the foreign gene has been modified by
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100.0%; Pred. No. 5.2e-16;
Live 0; Mismatches 0;
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Crop plant; polyadenylation signal; substitution; ferric reductase; iron;
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signals contained within the coding sequence are substituted with alterative codons for expression in higher plants. Oligonuleotides AA259031-259060 were used as overlapping oligonucleotide primers to generate a plant codon-optimised yeast ferric reductase (FREI gene; AA259028) in which putative polyadenylation signal and poly(A) addition sites are removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired foreign gene, especially to improve iron absorption efficiency in crop
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plant; polyadenylation signal; substitution; ferric reductase; iron;
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sites are removed by nucleotide substitution. The method allows the production of transformant plants with improved expression of a desired coreign gene, especially to improve iron absorption efficiency in crop
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The invention relates to a method of transforming a higher plant with a foreign gene in which the polyadenylation signal region contained in the nucleotide sequence of the foreign gene has been modified by nucleotide substitution to give a sequence not having this function, in such a way that the function of the foreign gene expression product is not substantially impaired. The foreign gene expression product is not substantially impaired. The foreign gene expression product is not substantially impaired of the foreign gene sequence are substituted with signals contained within the coding sequence are substituted with signals contained within the coding sequence are substituted with stransformers for alterative codons for expression in higher plants. Oligonuleotides AAS59031-S59060 were used as overlapping oligonucleotide primers to generate a plant codon-optimised yeast ferric reductase (FREI gene; AAS59028) in which putative polyadenylation signal and poly(A) addition sites are removed by nucleotide substitution. The method allows the constant of transformant plants with improved expression of a desired constant of the substitution of the sites are removed to the sites are removed to the sites are substituted of 
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SUMMARIES

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Description	B31006 Method form M86908 S. cerevisi U14913 Saccharomyc A86082 Sequence 74 AR155575 Sequence E66100 Genome DNA D83181 Candida a A8594 Sequence 63 AR15546 Sequence B31010 Method for B31010 Method for B31012 Method for B3102 Method for B3103 Method for B3103 Method for B3101 Method for	PAT 07-FEB-2001 is transformed plant and gene is transformed plant and gene
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1 (bases 1 to 3264)
Dancis, A., Roman, D. G., Anderson, G. J., Hinnebusch, A.G. and Klausner, R.D.
                                                                                                                   2040
                                                         2040
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="confers iron regulated activity to heterologous
                   TGGGTCATCAGTGGAGGATACAAACTCAGATGAGTCCCACTAAGGGTTTCGATGACAAGGA 1860
                                                                                              Ferric reductase of saccharomyces cerevisiae: Molecular characterization, role in iron uptake, and transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              end
                                                                                                                                               2041 GATAGATGTCGAACTAGAGGAGGAGAGTTTTACTTGGTAAGAGCTCAAGCTT 2092
                                                                                                                                     gatagatgtcgaactagaggaggaggttttacttggtaagagctcaagctt 2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="esential for ferric reductase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="5' end mapped by primer extention, 3'
from mRNA size"
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92237270
                                                                                                                                                                                                 YSCFREIA 3264 bp DNA PLN
S. cerevisiae ferric reductase gene, complete cds.
M86908
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/db_xref="taxon:4932"
1. 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ferric reductase"
/protein_id="AAA34608.1"
/db_xref="GI:171521"
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Saccharomyces cerevisiae
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1. .3264
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/gene="FRE1"
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                                                                             974 CAATATGGTTAGAACCCGTGTATTATTCTGCTTATTTATATCTTTTTTTGCTACGGTTCA 1033
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                          Indels
                        0; Mismatches 520;
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DB
Score 1244;
Pred. No. 0;
59.5%;
75.0%;
Query Match 59.5
Best Local Similarity 75.0
Matches 1556; Conservative
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us-09-646-825-1.rge

22-AUG-1997

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baker's yeast strain-5288C (AB972).

Baccharomyces cerevisiae

Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaces;

Saccharomycetales; Saccharomycetaces;

Saccharomycetales; Saccharomycetaces;

Saccharomycetales; Saccharomycetaces;

Saccharomycetales; Saccharomycets.

I (bases 1 to 38868)

Saccharomycetales; Saccharomyces;

Ansorge,W., Benes,V., Bruckner,M., Dellus,H., Dubols,E.,

Dusterhoft,A., Entlan,K.D., Floeth,M., Goffeau,A., Hebling,U.,

Heumann,K., Heusser,Neizeal,D., Hilbert,H., Hilger,F., Kleine,K.,

Kotter,P., Louis,B.J., Messenguy,F., Mewes,H.W., Miosga,T.,

Rotter,P., Louis,B.D., Purnellela,B., Rechmann,S., Rieger,M.,

Rotte,M., Rose,M., Scharfe,M., Scherens,B., Scholler,P.,

Schwager,C., Schwarz,S., Underwood,A.P., Urrestarazu,L.A.,

vandenbol,M., Verhasselt,P., Viernedeels,F., Voet,M., Volckaert,G.,

Voss,H., Wambutt,R., Wedler,E., Wedler,H., Zimmermann,F.K.,

Zollner,A., Hani,J. and Hoheisel,J.D.

The nucleotide sequence of Saccharomyces cerevisiae chromosome XII

By 171327
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/gene="YLR192C"
/note="Weakly similar to protein of unknown function from Halobacterium halobium (SwissProt accession number P13043)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"Pas20p: component of peroxisomal protein import
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Genetics, Washington University, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL: http://genome-www.stanford.edu/e-mail: yeast-curator@genome.stanford.edu.
Location/Qualifiers
1. .3868
/organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (22-AUG-1997) Saccharomyces Genome Database
Sequenced by:
                                                        Saccharomyces cerevisiae chromosome XII cosmid 8167.
U14913 X13138
U14913.1 GI:544497
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4 (bases 1 to 38868)
Cherry, J.M.
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3 (bases 1 to 38868)
Waterston, R.
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/note="YLR200W; homology to mouse KE2; contains a putative
leucine-ripper motif; homolog of a component of the bovine
NABC complex"
                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MAPIEYLLFEEPTGYAVFKVKLQQDDIGSRLKEVQEQINDFGAF
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AKVKFSYQKNDNHILQAIALLDQLDKDINFFAMRVKEWYGHIFPELAKLYDNYTFAK
LVLFIKDKASLNDDSLHDLAALLNEDSGIAQRVIDNARISMGQDISETDMENVCVFAQ
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LVAPSEGPNGFEKLSLSDMGSLVDLCGQWLGFEPSRYSEECYRLWRCDSAAIGAQSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVASLADYRRQLYDYLCEKMHTVAPNLSELĪGEVIGARLISHĀGSLTNLSKQAASTVO
TIGAEKALFRALKTKORPRVGLIYBGFISKASAKNKKRISTSRTLANKSMASRIDNY
SEEDSAVFGSYLK KOVEGRLEFYNTGKFTLKNELA IOBAMELYNKDKPAAEVBETKEK
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IFSLSFPSFLHHHLLIFSSLRIPFPWFLPLLQLVYLCYKVPWLLEWLHSSKLAYQCC
                                                                                                                                                            /note="YLR197W; homology to microtubule binding proteins; wild-type suppresses toxicity of GAL4-I-Kappa-B alpha in yeast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 atcgagggtacactcatctccacttcatgcatttctcaggctgcactgtaccagttcgg 135
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complement(8912. .9271)
/gene="YLR198C"
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10638. .10982
/gene="YKE2"
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                                                                              7723. .9237
/gene="SIK1"
7723. .9237
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                                                         EGGDEHDDMA"
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Matches 1556; Conserv
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OGGGNLFTRLLKKSGKLPTWYRPFLRGITETWIIEVSVVNPANSTMRYTRNLDHTG
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AFVIQKLEEARNPQF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-*Nmtlp: N-Myristoyltransferase"
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//db_xref=*G1:54511.
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(COMPLEMENT (1635. . 2162)
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VNGKVASVMSNITNGAFAGTHIAYGAGAFAVGALLL"
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IYVYDDGAGFHSSDIPVEEGDEADPDVARGLVRDPALYVHHDLMLPAFPLCVEWLDYK
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TILNNTKYKDLGIGYLYYYATDADFQFKDRFDPKATKALKTRLCELIYDACILAKNAN
MDVFNALTSQDNTLFLDDLKFGPGDGFLNFYLFNYRAKPITGGLNPDNSNDIKRRSNV
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/note="YLR195C"
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5594. .7324
/gene="PWP1"
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ir Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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ind Roselences of Ashbya gossypii and uses thereof 1515 agaacaacaacatcactttctactcatgcggaccagcgactttcaatga 1995 accataccgttgattgcaagattttcttagagggaccatatggcgtaac 1575 ttgccaaacttaagagaaatctagtaggagtagctggggcttggggt 1635 acceccatttegtagaatgeettagattgeetageactgateaactgea 1695 ttaacaagagccagacctcaaagagctagtgagatcagagatcaaatt 1935 atgoagttgtacaaggtatcgattctagtctgaagatagatgtcgaact 2055 21-JAN-2000 acgicaaagciaacaagggcattacgagagiactictiagcaaagitici PAT 694 bp DNA 741 from Patent EP0866129. GI:6734681

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                                                                                                                                                         1006 ctacttcagatggggaatagtagccacaattcttatgtccatcatcatttccagtccga 1065
                                                                                                                                                                                                         1066 gaaggtetteaggaacegaggttatgaaatettettaettateacaaagecatgaacat 1125
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                                                                                                                                      Gaps
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                                                                                                                                      12;
                                                                                                             Length 694;
                                                                                                                                   Indels
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                                                                                                          7.1%; Score 147.6; DB 6;
54.6%; Pred. No. 4.7e-32;
tive 0; Mismatches 274;
                     1. .694
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/db_xref="taxon:33169"
a 154 c 189 g 187 t
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Sequence 741 from patent US 6239264.
AR155575.1 GI:15123628
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Location/Qualifiers
                                                                                                                      Best Local Similarity 54.6
Matches 344; Conservative
CIBA GEIGY AG
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1366 ttcaccaaaatcagcctggttctacagttttcaatctcatccttcacagtcctatcaga 1425
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Peter, P.R. P., Steiner, C.M., Juergen, W.P.K.K. and Rebishun. Genome DNA sequence of Ashbya gossypii and use thereof Patent: JP 1999225770-A 740 24-AuG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1066 gaaggtetteaggaaccgaggttatgaaatettettaetteacaaagecatgaacat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1426 aaggcacagagatcctaacaacccagatcaactaactatgtacgtcaaagctaacaggg
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Genome DNA sequence of Ashbya gossypii and use thereof
E66100
E66100.1 GI:13020441
                                                                                                                                                                                               Length 694;
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                                                                                                                                                                                         Score 147.6; DB 6;
Pred. No. 4.7e-32;
0; Mismatches 274;
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Location/Qualifiers
1. .694
/organism="unknown"
a 154 c 189 g
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Best Local Similarity 54.6%;
Matches 344; Conservative
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unclassified
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06-FEB-1999

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/ CLANSIALLON="WIESKHAKYDKIQAEEKTNGTEYAKMTTKSSSGSKTSTSASKS
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QAOGAIGFYTGGHPAMVDELRFAVTQNLNVSKHRVEVHEQLQTWA"

58 a 58 3 C 601 9 1015 t
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Submitted (19-JAN-1996) to the DDBJ/EMBL/GenBank databases. Toshiko
Okabe, Yokohama City University, School of Medicine, Department of
Hygiene; 3-9 Fukuura, Kanazawa-ku, Yokohama, Kanagawa 236-0004,
Japan (E-mail:toshiko@med.yokohama-cu.ac.jp, Tel:BI-45-787-2606,
Fax:81-45-786-5219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 3084)
Yamada-Okabe,T.
Isolation of mRNA capping enzyme from Candida albicans, similar but
distinct genome organization between Candida albicans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada-Okabe,H.
Isolation of the mRNA-capping enzyme and ferric-reductase-related genes from Candida albicans
Microbiology 142 (Pt 9), 2515-2523 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada-Okabe, T., Shimmi, O., Doi, R., Mizumoto, K., Arisawa, M. and
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Saccharomycetales; mitosporic Saccharomycetales; Candida
1 (bases 1 to 3084)
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complete cds.
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Pred. No. 9.7e-18;
0; Mismatches 381;
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/transl_table=12
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Matches 344; Conservative 0
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PD 24-AUG-1999
PF 05-JAN-1998 JP 1998076818
PR 31-DEC-1996 CH 16/97
PI 'PETER PHILLIPSEN, REINER POHLMANN, SABINE STEINER, CHRISTINE MORE, PI JUERGEN WENDLAND, PHILLIP KUNEHITTORU, CORINNE REBISHUN PC C12N15/09, C12N11/15, C1201/18, C12
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Candida albicans cfll gene for ferric reductase.
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/organism-"candida albicans"
/db_xref="taxon:5476"
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CTSTGKRSTWHNCYCKTDAGFGTISDCLVRGFNNRTNIISRFTESCHMTESKFHAKTD
KISAEFKTNGTEYAKMTKSSGGKTSASASKSSKSTGSSNASKSSTNAHGSNSSTSS
TSSSSSKSGKGNSGTSTTETTTPLLIDYKRFTPYKDAYOMSNNNFNLSINYGSGLLG
YWAGILAIFANMIKKMFPSLINYLSGSISNLFRKHLFLPATFRKKKAOFFSIGVYG
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   sequence is in conflict with the conceptual
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Pred. No. 3e-17;
0; Mismatches 382; Indels 6
                                                                                                                                    /codon=(seq:"cag",aa:Ser)
/product="ferric reductase"
/protein_id="cab45649.1"
/db_xref="GI:S139350"
/db_xref="SPTREMBL:09Y861"
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                                                                      /codon_start=1
/transl_table=12
'note="Protein
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1 (bases 1 to 711)
Philippsen, P., Pohlmann, R., Steiner-Lange, S., Mohr, C., Wendland, J., Knechtle, P. and Rebischung, C. Genomic DNA sequences of ashbya gossypii and uses thereof Patent: US 6239264-A 633 29 MAY-2001;
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 ctcgagaacaacatcactttctactcatgcggaccagcgactttcaatgacgacttt
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Eukaryota: Fungi: Ascomycota: Saccharomycotina; Saccharomy Eukaryota: Fungi: Ascomycota: Saccharomycetales; Eremotheciaceae; Eremothecium.

1 (bases 1 to 711)

Mohr,C. and Knechtle,P.
Genomic DNA sequences of Ashbya gossypii and uses thereof Patent: EP 0866129-A 633 23-SEP-1998;
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Location/Qualifiers
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PD 05-OCT-1999

PF 24-MAR-1998 JP 1998096637

PR SATOSHI MORI, HIROYUKI OKI, NOBUHITO

YAMAGUCHI

PC (C12N15/09, A01H5/00, C12N5/10, C12P19/PC

PC (C12N5/10, C12R1:91), C12N15/00, C12N5/10, C12N5
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    .83
    /organism="unidentified"

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16/97

PI PETER PHILLIPSEN, REINER POHLMANN, SABINE STEINER, CHRISTINE MORE, PI JUERGEN WENDLAND, PHILLIP KUNEHHITORU, CORINNE REBISHUN PC C12AN15/09, C12AN1-5/09, C12AN1-5/09, C12AN1-5/09, C12AN1-5/00, C12AN-5/00, C12A
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S Peter, P.R.P. P., Steiner, C.M., Juergen, W.P.K.K. and Rebishun. Genome DnA sequence of Ashbya gossypii and use thereof
L Patent: JP 1999225770-A 632 24-AUG-1999;
NOVARTIS AG
OS PAG1427RP PN 19199225770-A/632
PD 24-AUG-1999
PF 05-JAN-1998 JP 1998076818
PR 31-DEC-1996 CH
I 16/97
PI PETER PHILLIPSEN REINER POHLMANN, SABINE STEINER, CHRISTINE MORE, PI JUERGEN WENDLAND, PHILLIP KUNEHHITORU, CORINNE REBISHUN
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                                                                                                                                                    DNA sequence of Ashbya gossypii and use thereof
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Pred. No. 3.8e-15;
0; Mismatches 268;
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/organism="unidentified"
/db_xref="taxon:32644"
a 193 c 167 g 18
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Satoshi,M.H.O.O. and Nakanishi,H.Y.
Method for transforming plant, the thus transformed plant and gene
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100.0%; Pred. No. 3.4e-13;
tive 0; Mismatches 0;
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SCIENCE & TECH AGENCY
OS Unidentified
PN JP 1999266876-A/7
PD 05-OCT-1999
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/organism="unidentified"
/db_xref="taxon:32644"
a 21 c 17 g 19
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/organism="unidentified"
/db_xref="taxon:32644"
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  Strandedness: Single;
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Satoshi,M.H.O.O. and Nakanishi,H.Y.
Method for transforming plant, the thus transformed plant and gene thereof
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Strandedness: Single;
Topology: Linear;
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4.0%; Score 83; DB 6; Length 83;
Best Local Similarity 100.0%; Pred. No. 3.4e-13;
Matches 83; Conservative 0; Mismatches 0; Indels
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Search completed: May 14, 2002, 07:24:06 Job time: 11053 sec



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May 14, 2002, 04:19:48; Search time 1786.89 Seconds (without alignments) 12580.611 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 11351937 seqs, 5372889281 residues OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 US-09-646-825-1 2092 Title: Perfect score: Scoring table: Sequence: Searched:

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em\_estfun:\* EST:\* Database :

gb\_est1:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AL408680 T7 end of AL42233 T3 end of AL42233 T3 end of AL421175 T7 end of AL411765 T7 end of AL455600 T3 end of AL452001 T7 end of AL45200 T3 end of AL45200 T3 end of AL42001 T7 end of AL42001 T7 end of AL42001 T7 end of AL42001 T3 end of AL42001 T3 end of Description CNSO6OYA AZ931275 CNSO6HK9 CNSO6HK9 CNSO6WLF CNSO6WLF CNSO6XPL CNSO6XPL CNSO6XPL AAS528430 CNSO6XPL CNSO1705 AAS5862 AAS58430 CNSO6WIF B Match Length DB 533.4 448.2 447.4 42.4 42.8 444.2 Score 187.4 Result Š. U O

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## ALIGNMENTS

CNSOGOYA 962 bp DNA GSS 05-JUL-2001 T7 end of clone AV0AA010B01 of library AV0AA from strain CBS 379 of Saccharomyces exiguus, genomic survey sequence. AL408680. AL408680.1 GI:12175485 GSS. Saccharomyces exiguus. Saccharomyces exiguus Eukaryota; Fungi; Ascomycota; Saccharomycetes;	Saccharomyoctales; Saccharomycetaceae; Saccharomyces.  1 (bases 1 to 962)  Bon, E., Neuveglise,C., Lepingle,A., Wincker,P., Artiguenave,F., Gaillardin,C. and Casaregola,S. Genomic exploration of the hemiascomycetous yeasts: 6. Saccharomyces exiguus FEBS Lett. 487 (1), 42-46 (2000) 2054016 2 (bases 1 to 962) Souciet,J.L., Augle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,	de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvegilse, C., Ozier-Kalogeropoulos, O., Potier, S., Sautin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000) 2058471 3 (bases 1 to 962) Genoscope Genoscope Direct Submission Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail):
RESULT 1 COSOSOVA/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS	TITLE JOURNAL MEDILINE REFERENCE AUTHORS TITLE JOURNAL

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segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces bayanus var. uvarum, Saccharomyces extrazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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/note="similar to Saccharomyces cerevisiae ORF YLR214w
FRE1 ; ferric (and cupric) reductase |"
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Saccharomycetales; Saccharomycetaceae; Saccharomycets.
I (bases 1 to 515)
Saccharomycetales; Saccharomyces.
Saccharomyces of a donnston, M. W. R., Waterston, R. H. and Johnston, M. Surveying Saccharomyces genomes to identify functional elements by comparative DNA sequence analysis
Unpublished (2001)
Contact: Johnston M
Department of Genetics
Washington University Medical School
Box 8212, 4566 Scott Ave., St. Louis, MO 63110, USA
Tel: 314 362 2735
Fax: 314 362 2735
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Pred. No. 2e-30;
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/strain="NRRL Y-1556 (CBS 398)'
/db_xref="taxon:27294"
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Class: random plasmid subclone.
Location/Qualifiers
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSO6ZHJ 966 bp DNA GSS 06-JUL-2001
T3 end of clone XAYOAA002F02 of library XAYOAA from strain CBS 6340
of Kluyveromyces thermotolerans, genomic survey sequence.
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I (bases 1 to 966)
Malpertuy, A., Llorente, B., Blandin, G., Artiguenave, F., Wincker, P. and Dujon, B.
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/note="similar to Saccharomyces cerevisiae ORF YLR215c strong similarity to rat cell cycle progression related
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Location/Qualifiers

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                                           CNSO6HK9 968 bp DNA GSS 17-JUN-2001
T7 end of clone ASOAA013A07 of library ASOAA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.
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//orde="similar to Saccharomyces cerevisiae ORF YLR213c {
similarity to UTR2 protein ]"
/eyidence=not_experimental
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                                                                                                                                                                                                                                                                                                  Bon, E., Neuveglise, C., Casaregola, S., Artiguenave, F., Wincker, P., Aigle, M. and Durrens, P. Genomic exploration of the hemiascomycetous yeasts: 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 968)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet,J.L., Aigle,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuvegilse,C., Ozler Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
                                                                                                                                                                                                         Saccharomyces bayanus
Eukaryota; Fung1; Ascomycota; Saccharomycot1na; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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FRE1 ; ferric (and cupric) reductase ]"
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/strain="CLIB 533"
/variety="uvarum"
/db_xref="taxon:4931"
/clone="ASOAA013A07"
/clone="Lib="ASOAA"
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0; Mismatches 65
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218 c 170 g 309 t
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FEBS Lett. 487 (1), 37-41 (2000)
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                                                                                                                   AL399103
AL399103.1 GI:12153151
                                                                                                                                                                                      Saccharomyces bayanus.
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Matches 135; Conservative
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RESULT CNSO6HK9
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L. Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) Fhis GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharcmyces bayanus var. uvarum, Saccharcmyces exiguus, Saccharcmyces servazzii, Zygosaccharcmyces rouxii, Saccharcmyces kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNSOGYLD 1015 bp DNA GSS 06-JUL-2001
T7 end of clone AYOAA010F03 of library AYOAA from strain CBS 6340
Of Kluyveromyces thermotolerans, genomic survey sequence.
AL411175.1 GI:12204374
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/note="similar to Saccharomyces cerevisiae ORF YLR214w |
FRE1 ; ferric (and cupric) reductase ]"
/evidence=not_experimental
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Eukaryota; Fungl; Ascomycota; Saccharomycetes;
Eaccharomycetales; Saccharomycetaceae; Kluyveromyces.

(bases 1 to 1015)
Malpertuy, A., Llorente, B., Blandin, G., Artiguenave, F., Wincker, P.
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Souclet,J.L., Algle,M., Artiguenave,F., Blandin,G.,
Souclet,J.L., Algle,M., Artiguenave,F., Casaregola,S.,
Bolothin-Fukuhara,M., Bon,E., Brottler,P., Casaregola,S.,
de-Montign,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozter-Kalogeropoulos,O., Potter,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
                                                                                                                                                           131
72 tccaatcgagcgctacactcacttcatgcatttctcaggctgcactgtaccagt
                                        132 teggatgeteaageaagteaagte------ttgetaetgeaagaacateaattggeteg
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/clone="AYOAA010F03"
/clone_lib="AYOAA"
                                                                                                                                                                                                                                                          Kluyveromyces thermotolerans.
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<320. .>844
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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strain CBS 7064
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Souchet,J.L., Aigle,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Sautin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
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1 (bases 1 to 958)
de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiquenave, F. and Potier, S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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                                                                                                                                                                                                                                                                                                                                                                                                   685 TCGSTGANACCAGACGGAGTTCGACTGGTACTACAAGAAGATGAAAGACCTGACGTTCTC 744
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                                                               Length 1015;
    others
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T7 end of clone AXOAA027B12 of library AXOAA from
of Pichia farinosa, genomic survey sequence.
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                                                            Score 53.4; DB 13;
Pred. No. 0.00091;
2; Mismatches 214;
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   232
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to Saccharomyces cerevisiae ORF YNR060w [ FRE4 ; strong similarity to Fre2p, and similarity to Fre1p
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/note="similar to Saccharomyces cerevisiae ORF YKL220c
FREZ; ferric (and cupilc) reductase ]
Similar to Saccharomyces cerevisiae ORF YOR384w [FRE5
strong similarity to ferric reductase Fre2p ]"
/evidence=not_experimental
a 222 c 246 g 226 t 27 others
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FRE3 ; strong similarity to ferric reductase Fre2p ]"
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    .958
    /organism="Pichia farinosa"
    /strain="CBS 7064"
    /db xref="taxon:4920"
    /clone="Ax0AA027B12"

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/note="end : T7"
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/organism="Kluyveromyces thermotolerans"
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TITLE
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AUTHORS
                                                1105
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PRES ; atrong miliarity to ferric reductase Fre2p ]
                                                                                               CNS079Q2 851 bp DNA GSS 08-JUL-2001
T3 end of clone BB0AA031C09 of library BB0AA from strain CBS 4732
of Pichia angusta, genomic entres commons
                                                                                                                                                                                                              Eukaryota; Fundi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
I (bases 1 to 851)
Blandin, 6, Llorente, B., Malpertuy, A., Wincker, P., Artiguenave, F. and Dujon, B.
                                                                                                                                                                                                                                                                                                                                              Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Casaregola, S.,
de-Montigny, J., Dujon, B., Burtens, P., Lepingle, M., Llorente, B.,
Malpertuy, A., Neuvegilse, C., Ozier Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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                                                                                                                                     Pichia angusta, genomic survey sequence.
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Pred. No. 0.024;
2; Mismatches 150;
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        1364 ctttcaccaaaatcagcctgg 1384
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50.8%;
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Best Local Similarity 50.8°
Matches 166; Conservative
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Direct Submission

L Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

L Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRX cedex, FRANCE. (E-mail:

2 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichla
angusta, Debaryomyces hansenli var. hansenli, Pichla sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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1 (bases 1 to 907)
Malpertuy,A., Llorente,B., Blandin,G., Artiguenave,F., Wincker,P.
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Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Souciet, J.L., Aigle, M., Artiguenave, F., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuvegilse, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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tattcacaaagccatgaacatcatgtttatcatagctatgtattaccattgccacacact 1164
                                                                                                                                                                                                                                     291 CGGATACCTGGAATGGACGTATGCCAGCATGGGAGTGTGGGCAATTGACAGAGTTTGGAG 350
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                                                                                  Genomic exploration of the hemiascomycetous yeasts: 10.
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FEBS Lett. 487 (1), 61-65 (2000)
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                           Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta, Liliopsida; Poales, Poaceae, Ehrhartoideae, Oryzeae; Oryza, (bases 1 to 805)
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                                                                                                                      Eukaryota; Metazoa; Arthrópoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="faxon:7227"
/clone_lib="DrosBAC"
/clone="BACN17H10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 44.2; DB 13;
Best Local Similarity 24.7%; Pred. No. 0.33;
Matches 64; Conservative 90; Mismatches 105;
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                                                                      fruit fly.
Plasmid Drosophila melanogaster
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                           GI:5627284
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Oryza sativa
                         AL107423.1
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                                                                                                                                                                                                                       Genoscope
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AQ858562/c
LOCUS
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                                                                                                                                                                                                                                             TITLE
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  ACCESSION
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                                                                                                                                                                                                                                                                                                                                           /note="similar to Saccharomyces cerevisiae ORF YNR060w [ FRE4 ; strong similarity to Fre2p, and similarity to Fre1p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /9. ..3881
/note="similar to Saccharomyces cerevisiae ORF YLL051c
FRE6 ; strong similarity to ferric reductase Fre2p ]"
/evidence=not_experimental
a 217 c 234 g 282 t 4 others
                                                                                                                                             /note="similar to Saccharomyces cerevisiae ORF YKL220c FRE2; ferric (and cupric) reductase ] similar to Saccharomyces cerevisiae ORF YOR381w [ FRE3
                                                                                                                                                                                                                  strong similarity to ferric reductase Fre2p | similar to Saccharomyces cerevisiae ORF YOR384w [ FRE5 strong similarity to ferric reductase Fre2p ]"
                                                                                                                                                                                                                                                                                                                                                                                                                                    <6. >950
/note="similar to Saccharomyces cerevisiae ORF YLR214w
FRE1 ; ferric (and cupric) reductase ]"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      978 gagtattccagtctcttgtaaggaaattctacttcagatgggaatagtagccacaattc 1037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           798 tgatggcaatcgctctttccccgtggtgtaccttttcggtatccggaacaaccccttca 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toccaatcaccggattgagctttagtactttcaacttttaccacaaatggtcagcatacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 TCCTATTICTAACAGTATTCACCCACACATTTCGATGCTTATGTACACTTATGCGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.3%; Score 47.4; DB 13; Length 987;
44.0%; Pred. No. 0.042;
tive 1; Mismatches 247; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence-not_experimental
                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                      /db_xref-"taxon:4916"
                                           /clone="AY0AA002H01"
/clone_lib="AY0AA"
/note="end : T7"
'strain="CBS 6340"
                                                                                                                                                                                                                                                                                                               <6. .>983
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1218 tctgccgaattgtacgtatcatc 1240
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268

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RESULT

388

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Indels

Length 1101;

240 others

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/organism="City2a Sativa"
//organism="City2a Sativa"
//cultivar="Nipponbare"
//dutivar="Nipponbare"
//do.rafe="texponsists"
//do.rafe="texponsists"
//clone="lib="CuGI Rice BAC Library (EcoRI)"
//clone="lib-"CuGI Rice BAC Library In the world Half of the world population side is a diploid plant (2n=24) with a happloid genome equivalent of 431 Mbp (Arumuganathan and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximentley 15 happoid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each contraining should colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatagatgtcgaactagaggaggagttttacttggtaagagc 2084
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                                                                                                                               Clemson University Genomics Institute
                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC/EST Resource Center
237 c 189 q 19
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High quality sequence stop: 406.
Location/Qualifiers
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Matches 134; Conservative
                                                                                                      Contact: Wing RA
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JOURNAL
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            AUTHORS
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/b_xref="taxon:575"
//db_xref="taxon:5759"
//clone_lib="Entamoeba histolytica Sheared DNA"
//clone_lib="Entamoeba histolytica Sheared DNA"
//clone_lib="Entamoeba histolytica Sheared DNA"
//clone_lib="taxon:5759"
//clone_l
                                                                                                                                                                                                                                                                                                 Entamoeba histolytica.

Entamoeba histolytica.

Eukaryota: Entamoebidae; Entamoeba.

Eukaryota: Entamoebidae; Entamoeba.

E I (bases 1 to 88)

L offus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1: MSS sheared DNA library

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medicad Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
                                                                         AZ528430 888 bp DNA GSS 03-NOV-2000
ENTCO24TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 CGTCTTCTTCATCGTCTTCTTCATCGTCTTCATCGTCTTCATCGTCTTCAT 200
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43.7%; Pred. No. 0.76;
tive 0; Mismatches 242; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 91
High quality sequence stop: 445.
Location/Qualifiers
1. .888
/organism="Entamoeba histolytica"
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AZ528430
AZ528430.1 GI:11080689
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L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
5 seqréfégenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                   CNSOGNMI 949 bp DNA GSS 04-JUL-2001
T3 end of clone AUGAA015D05 of library AUGAA from strain CBS 3082
Of Saccharomyces kluyveri, genomic survey sequence.
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FEBS Lett. 487 (1), 3-12 (2000)
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 949)
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1087 ttatgaaatcttcttacttattcacaaagccatgaacatcatgtttatcatagctatgta 1146
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/clone="AU0AA015D05"
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Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: nbw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                               811 tcttttccccgtggtgtaccttttcggtatccggaacaaccccttcatcccaatcaccgg 870
                                                                                                                                                                                          871 attgagctttagtactttcaacttttaccacaaatggtcagcatac----gtctgcttca 926
                                                                                                                                                                                                                                                                                                                                                                     381 MTAGAAACAAWCTACTWWTATRACATACCACAAGWGGATTGCATACAGTATGCTATATCA 322
                                                                             Gaps
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACRO8K10"
2.0%; Score 42.8; DB 13; 44.9%; Pred. No. 0.78;
                                                                  12; Mismatches 169;
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Candida tropicalis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F.
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                                                                                                                          605 aacgagagactttctatctttggaaacgtttgccattcaactttacaactcgaggcaaa 664
                                                                                                                                                                                         536 АМАТАААТWTWWTWTYTTWAAWATAAAMCMAAWYYHTYTTYTYHYYTYWTYTMTWHYH 595
                                                                                Gaps
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2
                                                   Length 1101;
 503 others
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                                                   Query Match 2.0%; Score 42.8; DB 13; Best Local Similarity 17.3%; Pred. No. 0.82; Matches 109; Conservative 252; Mismatches 264;
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similar to Saccharomyces cerevisiae ORF VNR060w [ FRE4 strong similarity to Fre2p, and similarity to Fre2p, and similarity to Fre2p, and similarity to Fre2p, and similarity to ferric reductase Fre2p]
strong similarity to ferric reductase Fre2p]
strong similarity to ferric reductase Fre2p]
strong similarity to ferric reductase Fre2p]
/evidence=not_experimental
a 173 c 235 g 345 t 3 others
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602677117F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4799501 5',
mRNA sequence.
BG714799
Souciet, J.L., Aigle, M., Artiguenave, P., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Libente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, C., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiasconycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1072 cttcaggaaccgaggttatgaaatcttcttacttattcacaaagccatgaacatcatgtt 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1192 ggctggcatcctctgcttcgacaggttctgccgaattgtacgtatcatgaacgg 1248
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52.0%; Pred. No. 2.5;
tive 0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Candida tropicalis"/strain="CBS 94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5482"
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/note="end : T3"
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs refmail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM10689 row: a column: 06

High quality sequence start: 10

High quality sequence start: 10

High quality sequence start: 10

High quality sequence story: 22.
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                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                             1 (bases 1 to 2149)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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/clone=lib="MYL/MGC_96"
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/lab_host="bH108"
                                        Homo sapiens
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ORIGIN
SOURCE
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AUTHORS
TITLE
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COMMENT
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Gaps ; cuery Match 2.0%; Score 41; DB 11; Length 2149; Best Local Similarity 51.4%; Pred. No. 3.3; Matches 95; Conservation

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1295 atcaagatctctgtcaagaagcctaagttcttcaagtatcaagtgggagcatttgcctat 1354

1355 atgtactttctttcaccaaaatcagcctggttctacagttttcaatctcatcccttcaca 1414

1415 giccialcagaaaggcacagagatcciaacaacccagaicaactaactatgiacgicaaa 1474 g ò

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1475 gctaa 1479 ò

1461 AATTA 1465

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